

Seq	Strid	Orig	ZScore	EScore	Len	Document
gb.est20:AA849015	+	843.00	1186.00	2.7e-57	623	AA849015.Estr191777
gb.est23:AAW02552	+	811.50	1155.02	1.4e-55	500	AAW02552.vu97604.x1
gb.est27:AT400249	+	819.50	1142.17	7.5e-55	591	AT400249.tg68601.x1
gb.est31:AAW08210	+	810.50	1142.51	7.1e-55	492	AAW08210.xb61f03.x1
gb.est34:AA806597	+	808.50	1140.41	9.8e-55	476	AA806597.vf35103.x1
gb.est34:AA806597	+	767.50	1081.80	1.7e-51	502	AA806597.vf35103.x1
gb.est20:AA881508	+	759.00	1068.11	1.0e-50	602	AA881508.vx119f05.x1
gb.est22:AA937508	+	757.00	1066.39	1.4e-51	426	AA937508.Ur-E1.gb-f-03-o-01.s1
gb.est33:AAW04732	+	754.00	1064.45	1.6e-50	422	AAW04732.Ur-M.H1.amc-e-06-o-00-u1.s1
gb.est33:AA873269	+	747.00	1053.70	6.3e-50	464	AA873269.vf41c08.x1
gb.est31:AA821316	+	722.00	1016.81	7.2e-48	457	AA821316.mu43f12.x1
gb.est28:AA505924	+	718.00	1013.90	1.0e-47	415	AA505924.v639608.x1
gb.est38:AAW048541	+	687.00	970.93	2.6e-45	389	AAW048541.Ur-M.BH1.alx-c-08-o-00-u1.s1
gb.est28:AA502911	+	680.00	960.98	2.6e-45	393	AA502911.Ur-R.C1.mr-f-07-o-00-u1.s1
gb.est16:AA547459	+	607.00	855.43	6.1e-39	475	AA547459.vf63908.s1
gb.est33:AA710434	+	600.00	843.32	1.2e-38	349	AA710434.Ur-R.AG1.aak-b-01-o-00-u1.s1
gb.est32:AA105051	+	592.50	833.31	9.2e-38	512	AA105051.o346c05.s1
gb.est39:AAW19108	+	582.00	821.05	5.7e-37	485	AAW19108.mf66003.x1
gb.est18:AAW051817	+	576.50	812.41	7.7e-36	533	AAW051817.vf203005.x1
gb.est38:AAW055217	+	558.50	790.83	7.9e-35	552	AAW055217.vf202802.x1
gb.est20:AA828319	+	558.00	780.35	2.9e-35	378	AA828319.ob55f04.s1
gb.est37:AA1966472	+	543.00	770.36	3.8e-34	312	AA1966472.vf896e10.x1
gb.est37:AA1671628	+	543.00	770.35	3.8e-34	312	AA1967070.w331f09.x1
gb.est33:AA134637	+	521.00	733.40	2.0e-32	313	AA134637.w44h11.x1
gb.est32:AA1215431	+	514.00	729.45	7.3e-32	315	AA1215431.Ur-H.B11.abd-l-h-09-o-00-u01.s1
gb.est24:AA12343585	+	497.00	706.52	1.6e-28	284	AA12343585.qh82602.x1
gb.est28:AAO20019	+	466.50	658.34	6.4e-28	493	AAO20019.mh48e1.x1
gb.est30:AA1563622	+	448.00	638.21	8.8e-27	436	AA1563622.vf50f03.x1
gb.est9:AA1166407	+	446.50	631.35	1.2e-26	265	AA1166407.mf939e12.x1
gb.est12:AA283034	+	442.00	628.62	3.0e-26	299	AA283034.z11ec10.s1
gb.est10:AA145823	+	435.50	615.14	1.7e-25	471	AA145823.mf68c10.x1
gb.est31:AA1701627	+	432.00	613.14	1.7e-25	281	AA1701627.tg39e02.x1
gb.est20:AA821494	+	422.00	597.01	1.7e-24	430	AA821494.vv59e03.x1
gb.est32:AA1742049	+	418.00	588.86	4.9e-24	560	AA1742049.vf338d03.x1
gb.est37:AA145298	+	408.00	587.98	1.0e-23	237	AA145298.Ur-R.EO.ce-e-11-o-01-u1.s1
gb.est9:AA118286	+	393.00	515.72	5.8e-20	337	AA118286.mf68f10.x1
gb.est20:AA886657	+	398.00	480.48	4.3e-18	360	AA886657.vf306f09.x1
gb.est30:AA886510	+	261.00	377.80	2.8e-12	198	AA886510.zx90a12.r1
gb.est19:AA788818	+	258.00	368.15	9.7e-11	350	AA788818.vf12a12.r1
gb.est38:AAW013268	+	254.50	353.89	4.7e-11	756	AAW019268.td51a04.x1

291 CATCAGCGGACGACGCTCTCTGAGCGCTGCTTACTGGGGAC 242

84 roLeuSerValHisGlyAlaHisGlyLeuArgLeuArgAlaGluProValGly 100
 241 CCTGTAGCGCGCATGGGGCCGACGAAACGGCTGCTGCGGAGCCCGTGGGC 192
 101 ThrPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeuSe 117
 191 ACCTTCTGTGGTGGCGACAGTCCGACGGAGACTGCTTCTTCGCGCTCAG 142
 117 rValIysMetAlaSerGlyProThrSerIleArgValHisPheGlnAlaG 134
 141 CGTGAAGATGGCTTCGGGGCCCGACGAGCATTCGTGCACTTCAGAGCCG 92
 134 lYArgPheHisIleuAspGlySerArgGlnThrPheAspCysLeuPheGlu 150
 91 GCCGCTTCCACCTGGAGCGGACGGCGGAGACCTTCGACTGCTTCGAG 42
 151 LeuLeuGluHisTyrValAlaAlaProArgArgMetLeu 163
 41 CTGCTGAGCACTACGTGGCGGCGCCCGCCGCACTGTTG 3

seq_name: gb_est38:AM025552

seq_documentation_block: 500 bp mRNA 27-OCT-1999
 LOCUS AM025552.1 NCI_CGAP_K143 Homo sapiens cDNA clone IMAGE:2528022 3'
 DEFINITION W07904.X1 NCI_CGAP_K143 Homo sapiens cDNA clone IMAGE:2528022 3'
 similar to TR:O35716 CYTOKINE INDUCIBLE SH2-CONTAINING
 PROTEIN 7 ; mRNA sequence.

ACCESSION AM025552
 VERSION AM025552.1 GI:5879082
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 500)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On Jun 5, 1998 this sequence version replaced gi:3187655.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILM at:
 www.bio.linn.gov/dbtrp/image/image.html

FEATURES
 SOURCE

Seq primer: -40UP from G1bco
 High quality sequence stop: 464.
 Location/Qualifiers
 1..500
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2528022"
 /clone_1lb="NCI CGAP_K143"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer,
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pT73 vector. mRNA
 source: 2 pooled kidneys. Library went through one round
 of normalization. Library constructed by Bento Soares and
 M. Fatima Bonaldo."

BASE COUNT 76 a 157 c 198 g 68 t 1 others

ORIGIN

alignment_scores:
 Quality: 819.50 Length: 165
 Ratio: 5.059 Gaps: 1
 Percent Similarity: 98.182 Percent Identity: 94.545

alignment_block:
 US-08-962-560a-4 x AM025552/rev ..

Align seg 1/1 to reverse of: AM025552 from: 1 to: 500

1 MetValAlaArgAsnGlnValAlaAlaAspAsnAlaIleSerProAla 17
 492 ATGTGTCACACACACACAGGTGGACCGGACATTCGATTCACACAGCAC 443
 17 acGluProArgArgArgSerGluProSerSerSerSerSerSerSer 34
 442 AGAGCGCCGAGCGGCGCCAGAACN...TCCCTCTTCTCTCTCTCTGC 396
 34 roAlaAlaProValArgProArgProCysProAlaValProAlaProAla 50
 395 CCGCGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 346
 51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArg 67
 345 CCGGCGGACACGCACTCCGCACTTCGTTGCAAGCGCGGATACCGGCG 296
 67 glierThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGly 84
 295 CATCAGCGCGCGCAGCGCGCTCTGAGCGCTCGCGGATTCACGCGGCG 246
 84 roLeuSerValHisGlyAlaHisGlyLeuArgLeuArgAlaGluProValGly 100
 245 CCTGTAGCGCGCATGGGGCCGACGAGCGCTGCGGCGGAGCCCGTGGGC 196
 101 ThrPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeuSe 117
 195 ACCTTCTGTGGTGGCGACAGCTCCGAGCACTTCTTCGCGCTTAG 146
 117 rValIysMetAlaSerGlyProThrSerIleArgValHisPheGlnAlaG 134
 145 CGTGAAGATGGCTTCGGGGCCCGACGAGCATTCGCTGCACTTCAGCGCG 96
 134 lYArgPheHisIleuAspGlySerArgGlnThrPheAspCysLeuPheGlu 150
 95 GCCGCTTCCACCTGGATGGACCGCGGAGAGCTTGACTGCTCTTCGAG 46
 151 LeuLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAla 165
 45 CTGCTGAGCACTACGTGGCGGCGCGCGCGCGCACTGCGGGGCC 1

seq_name: gb_est27:A1400249

seq_documentation_block: 591 bp mRNA 30-MAR-1999
 LOCUS A1400249 t968d01.x1 Soares_NHMPU.S1 Homo sapiens cDNA clone IMAGE:2113921
 DEFINITION t968d01.x1 Soares_NHMPU.S1 Homo sapiens cDNA clone IMAGE:2113921
 3 similar to TR:O15097 O15097 JAB, PATITAL CDS ; contains MER22.B2
 MSN1 repetitive element ; mRNA sequence.

ACCESSION A1400249
 VERSION A1400249.1 GI:4243336
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 591)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On Mar 20, 1998 this sequence version replaced gi:2980432.


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1 MetValAlaArgAnGlnValAlaAlaAspAsnAlaIleSerProAlaAl 17
|||||
492 ATGTACACACACACAGGAGGCGGACATCACTCCACAGAGC 443
17 AGLProArgArgArgSerGluProSerSerSerSerSerSerSer 34
|||||
442 AGAGCCCGGAGCGGCGGAGAGACT...TCTCTCTCTCTCTCTCTCT 396
34 rolaAlaProValArgProArgProCysProAlaValProAlaProAla 50
|||||
395 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 346
51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArg 67
|||||
345 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 296
67 gileThArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGly 84
|||||
295 CATACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 246
84 roLeuSerValHisGlyAlaHisGlyAlaArgLeuArgAlaGluProValGly 100
|||||
245 CCGTACGCGTGCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 196
101 ThrPheLeuValArgAspSerArgGlnArgAsnGlyPhePheAlaLeu 117
|||||
195 ACCTTCTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 146
117 rValMetAlaSerGlyProThrSerIleArgValHisPheGlnAlaG 134
|||||
145 CGTGAAGATGGCTCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 96
134 lYarGpPheHisLeuAspGlySerArgGluThrPheAspCysLeuPheGlu 150
95 GCCCTTTCACCTGTGATGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 46
151 LeuLeuGlnHisTyrValAlaAlaProArgArgMetLeuGlyAla 165
45 CTGTGGAGCACTACGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1
seq_name: gb_est31:AI683421

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seq_documentation_block: 476 bp mRNA EST 26-MAY-1999
LOCUS AI683421 tw51a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2263192 3'
DEFINITION Similar to TR:015097 015097 JAB, PARTIAL CDS ;, mRNA sequence.
ACCESSION AI683421 GI:4893603
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 476)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
REFERENCE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1998 this sequence version replaced gi:3137658.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbfp/image/image.html
Seq primer: -40UP from G1bco

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High quality sequence stop: 433.

FEATURES

Location/Qualifiers

1..476
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2263192"
/clone_11b="NCI_CGAP_Ut1"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-Sport6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"

BASE COUNT 70 a 154 c 197 g 54 t 1 others

alignment_scores:

Quality: 808.50 Length: 159
Ratio: 5.150 Gaps: 1
Percent Similarity: 98.742 Percent Identity: 96.226

alignment_block:

US-08-962-560A-4 x AI683421/rev ..

Align seg 1/1 to reverse of: AI683421 from: 1 to: 476

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16 AlAlaGluProArgArgSerGluProSerSerSerSerSer 32
476 GCAGCAGAGCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 430
32 rSerProAlaAlaProValArgProArgProCysProAlaValProAlaP 49
429 CTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 380
49 rolaProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyr 65
379 CGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 330
66 ArgArgIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyr 82
329 CGGCGCATCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 280
82 pGlyProLeuSerValHisGlyAlaHisGlyAlaArgLeuArgAlaGluPro 99
279 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 230
99 aGlyThrPheLeuValArgAspSerArgGlnArgAsnGlyPhePheAla 115
229 TGGGCACTCTCTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
116 LeuSerValHisMetAlaSerGlyProThrSerIleArgValHisPheG 132
179 CTTAGCGGTGAAGATGGCTCGGAGCGGCGGCGGCGGCGGCGGCGG 130
132 naAGlyArgPheHisLeuAspGlySerArgGluThrPheAspCysLeuP 149
129 GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 80
149 heGluLeuLeuGlnHisTyrValAlaAlaProArgArgMetLeuGlyAla 165
79 TCAGAGCGTGCAGCACTACGTGGCGGCGGCGGCGGCGGCGGCGGCGG 30
166 ProLeuArgGlnArgArgValArgPro 174
29 CCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3
seq_name: gb_est34:AI806697

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seq_documentation_block: 502 bp mRNA EST 07-JUL-1999
LOCUS AI806697 tw35f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
DEFINITION

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IMAGE:2357597.3' similar to TR:O15097 O15097 JAB, PARTIAL CDS ;,
 mRNA sequence.
 ACCESSION A1806697 GI:5393263
 VERSION A1806697.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 502)
 NCBI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 On Jun 5, 1998 this sequence version replaced gi:3187434.
 CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LINTL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40UP from G1bco
 High quality sequence stop: 457.
 Location/Qualifiers
 1..502
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2357597"
 /clone_1lb="Soares.NFL.T.GBC.S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI-CGAP GCBI) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 1.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 78 a 157 c 198 g 69 t
 ORIGIN
 alignment_scores:
 Quality: 767.50 Length: 161
 Ratio: 4.984 Gaps: 2
 Percent Similarity: 95.652 Percent Identity: 91.925
 alignment_block:
 US-08-962-560A-4 x A1806697/rev ..
 Align seg 1/1 to reverse of: A1806697 from: 1 to: 502

285 CAGCGCGCTCTGAGACCGCCGCGGATTCACCTGGGGCCCCCTAGCGTGC 236
 88 TsclyAlaHISGLuArgLeuArgAlaGluProValGlyThrPheLeuVal 104
 235 ACGGGCGCAGACGCGGCTCGCGCGAGCCCGTGGCACCCTCTGCTG 186
 105 ArgAspSerArgGlnArgAsnGlyPhePheAlaLeuSerValysMetAl 121
 185 CGCGACAGCCGCGAGCGGAACCTGTTTTCGCCCTTAGCGTGAAGATGC 136
 121 aserGlyProThSerLeuArgValHisPheGlnAlaGlyArgPheHis 138
 135 CTCGGACCCAGCAGCATCCGCGCTTCAGCGCGCGCTTCACC 86
 138 euAspGlySerArgGluThrPheAspCysLeuPheGluLeuGlnHis 154
 85 TGATGCGACACCGCGAGAGCTGACCTCTCGAGCTGCTGAGACAC 36
 155 TyrValAlaAlaProArgArgMetLeuGly 164
 35 TACGTGGCGGAGACCGCGCCGACCTGCTG 5
 seq_name: gb_est20:A881502
 seq_documentation_block: 602 bp mRNA EST 26-MAR-1998
 LOCUS A881502
 DEFINITION vx19f05.r1 Soares 2NBMT Mus musculus cDNA clone IMAGE:1264929 5'
 similar to TR:O35716 O35716 SUPPRESSOR OF CYTOKINE SIGNALING-1.
 [1] ;, mRNA sequence.
 ACCESSION A881502
 VERSION A881502.1 GI:2990812
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 602)
 Auerbach, S., Knudsen, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Scheibenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 On Sep 12, 1996 this sequence version replaced gi:1398104.
 CONTACT: Maira M/Mouse EST Project
 WASHU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LINTL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:667481
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 459.
 Location/Qualifiers
 1..602
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1264929"
 /clone_1lb="Soares 2NBMT"
 /sex="male"
 /tissue="thymus"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer 15'
 TGTACCAATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTTCTTTTCTTTT

3'): double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 76 a 243 c 181 g 101 t 1 others
ORIGIN

alignment_scores:
Quality: 759.00 Length: 147
Ratio: 5.234 Gaps: 0
Percent Similarity: 98.639 Percent Identity: 97.279

alignment_block:
US-08-962-560A-4 x AA881502 ..

Align seg 1/1 to: AA881502 from: 1 to: 602

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1 MetValAlaArgAsnGlnValAlaAlaAspAsnAlaIleSerProAlaAla 17
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162 ATGTACACAGCAACAGGTGCAGCCGACATGCGATCCCGGAGC 211
|||||
17 AGUProArgArgSerGluProSerSerSerSerSerSerSerSer 34
|||||
212 AGAGCCCGGACGGGGGTACAGCCCTCTGCTCTCTCTCTCTCTCT 261
|||||
34 roAlaAlaProValAlaArgProArgProCysProAlaValProAlaProAla 50
|||||
262 CACGGGCCCCGGTGGCGTCCCGGCGCCCGGCGGTCCAGCCAGCC 311
|||||
51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArg 67
|||||
312 CCGTGGGAGNCCTCACTCCGACCTTCGCTCCGACATCCATTAACGGCG 361
|||||
67 gileThArgThrSerAlaLeuAspAlaCysGlyPheTyrTrpGly 84
|||||
362 CACACCGGACCAAGCCGCTCTCTGAGCGCTCGGCTTATGGGAGC 411
|||||
84 roLeuSerValHisGlyAlaHisGlyAlaArgLeuAlaGluProValGly 100
|||||
412 CCTGAGCGGTGCACAGGGCGCCAGAGCGGCTGCGTCCGAGCCCGTGGCG 461
|||||
101 ThrPheLeuValAlaArgSerArgGlnArgAsnCysPheAlaLeu 117
|||||
462 ACCTTCTGTGGCGGACAGTCCGACAGGAGACTGCTTTCGGGCTCAG 511
|||||
117 ValIysMetAlaSerGlyProThrSerIleArgValHisPheGlnAla 134
|||||
512 GCTGAGATGGCTTCGGGGCCCAAGACATCCGCTGCACTTCAGAGCGC 561
|||||
134 LysArgPheHisLeuAspGlySerArgGluThrPheAspCys 147
|||||
562 GCGGCTTCCACTTGAGCGGACGCGGAGACTTCGACTGC 602
|||||

```

seq_name: gb_est27.AA957508

seq_documentation_block:

LOCUS AA957508 426 bp mRNA EST 09-MAR-1999
DEFINITION UI-R-EI-gb-f-05-0-UI.s1 UI-R-EI Rattus norvegicus cDNA clone
UI-R-EI-gb-f-05-0-UI 3', mRNA sequence.
ACCESSION AA957508
VERSION AA957508.1 GI:4277398
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 426)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On May 7, 1998 this sequence version replaced gi:3121203.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics The following repetitive elements were
found in this cDNA sequence: 366-425, >CC-rich#low_complexity
Seq primer: M13 Forward.

FEATURES

source

1..426

Location/Qualifiers

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-EI-gb-f-05-0-UI"

/clone_id="UI-R-EI"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-EI
library is a subtracted library derived from the UI-R-EI
library. The UI-R-EI library consisted of a mixture of
individually tagged normalized libraries constructed from
8, 12 and 18-day embryo. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dt track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-EI) was constructed as follows: PCR
amplified cDNA inserts from a pool of UI-R-EI clones from
which 3' ESTs had been derived was used as a driver in a
hybridization with the UI-R-EI library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-EI
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)."

BASE COUNT 72 a 139 c 167 g 48 t
ORIGIN

alignment_scores:

Quality: 757.00 Length: 142
Ratio: 5.331 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.592

alignment_block:
US-08-962-560A-4 x AA957508/rev ..

Align seg 1/1 to reverse of: AA957508 from: 1 to: 426

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33 serProAlaAlaProValAlaArgProArgProCysProAlaValProAlaBr 49
|||||
426 TCGCGGGGGGGCGGGCGGGGTCCCGGGGTCCCGGGGTCCCGGGCGCC 377
|||||
49 oAlaProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyr 66
|||||
376 GGCTCCGGCGGACACTTCATCCGACACTTCGCTCCAGCTGTGATACC 327
|||||
66 rGArgLleThArgThrSerAlaLeuAspAlaCysGlyPheTyrTrp 82
|||||
326 GCGGCTACAGCGGACAGCGCTCTGAGAGCGCTGGGCTTACTGG 277
|||||
83 GlyProLeuSerValHisGlyAlaHisGlyAlaArgLeuAlaGluProVal 99
|||||

```

```

|||||
276 GACCCCTGACGCTGATGGGGCGACAGCGCTGCGACGCCGT 227
99 1G1YThPheUValAArgAspSerArgGlnArgAsnCysPheAla 116
226 GGGCACCTTCTGTGGCGCGACAGTGGCCAGCGAATCTTCTTCGCGC 177
116 euSerValyMeAlaSerGlyProThrSerLeArgValHisPheGln 132
176 TCAGGTAAGATGGCTTCGGGCCCCACAGACATTCGTGACTTCAG 127
133 AlaGlyArgPheHisLeuAspGlySerArgGlnThrPheAspCysLeuPh 149
126 GCCGGCCCTTCACCTCGACGCGCGCGCGACCTTCGACTGCTT 77
149 eGluLeuLengluHisTyrValAlaAlaProArgArgMetLeuGlyAlaP 166
76 CGAGCTGCTGAGCAGCTACGTGGCGCGCGCGCGCATGTGGGGGCC 27
166 roLeuArgGlnArgArgValArgPro 174
26 CACTGGCGCAGCGCGCGCTGGCGCG 1

```

seq_name: gb_est38:AM047382

seq_documentation_block:

LOCUS AM047382 422 bp MRNA EST 18-SEP-1999

DEFINITION UI-M-BH1-ame-e-06-0-UI.s1 NIH_BMAP_M.S2 Mus musculus cDNA clone

ACCESSION AM047382

VERSION AM047382.1 GI:5907911

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 422)

Bonaldi,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

genome Res. 6 (9), 791-806 (1996)

JOURNAL 97044477

MEDLINE On Jun 5, 1998 this sequence version replaced gi:3189644.

COMMENT Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mestr@mail.nih.gov

Oligo-dT track not found. Not 1 site shown in beginning of sequence

is likely internal to the message. cDNA library preparation: M.B.

Soares Lab clone distribution: NIH BMAP cDNA clones will be made

available by the means that is soon to be determined. When NIH

determines the means for distribution of the BMAP cDNA clones, this

record will be updated accordingly when that means is determined.

Seq primer: M13 forward

POLYA-No.

FEATURES

source

1. .422

Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-BH1-ame-e-06-0-UI"

/clone_lib="NIH_BMAP_M.S2"

/dev_stage="27-32 days"

/note="Vector: pT73D-Pac (Pharmacia)"

/polylinker: Site_1: Not I; Site_2: Eco RI; The

NIH_BMAP_M.S2 library is a subtracted library derived from

NIH_BMAP_M.S1, which in turn is a subtracted library

derived from a mixture of normalized libraries from ten

regions of the mouse brain (cerebellum, brain stems,

olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M.S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.

BASE COUNT 68 a 135 c 169 g 50 t

ORIGIN

alignment_scores:

Quality: 754.00 Length: 140

Ratio: 5.386 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-962-560a-4 x AM047382/rev ..

Align seg 1/1 to reverse of: AM047382 from: 1 to: 422

```

35 AlaAlaProValArgProArgProCysProAlaValProAlaProAlaPr 51
|||||
420 GCGGCCCCCGTGGCTCCCGGCGCTGCGCGGCTCCCGACGCCAGGCC 371
51 OGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArgArg 68
370 TGGCGACACTCATTCCGACACTCCGCTCCCACTCCGATACCGGCGCA 321
68 IeThrArgThrSerAlaLeuAspAlaCysGlyPheTyrTrpGlyPro 84
320 TCACGCGGACGAGCGCGCTCCTGAGCGCGCTGCTTATTTGGGAGACC 271
85 LeuSerValHisGlyAlaHisGlyArgLeuArgAlaGluProValGlyTh 101
270 CTGAGCGGCGACGGGGCGCGACGAGCGGCTGCTCCGACGCCGtGGGCAC 221
101 rPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeuSerV 118
220 CTCTGTGGTGGCGGACAGTCCCAAGCAAGCAACTGCTTCTTCGCGTCAAGC 171
118 alyMetAlaSerGlyProThrSerLeArgValHisPheGlnAlaGly 134
170 TGAAGATGGCTTCGGGCGCCGACGAGCATCCGCGTGCACCTTCAGCGCGC 121
135 ArgPheHisLeuAspGlySerArgGlnThrPheAspCysLeuPheGlu 151
120 CGCTTCACCTTGACGCGGACGCGCGGAGACCTTCGACTGCTTTCGAGACT 71
151 uLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProLeuA 168
70 GCTGAGAGACTACGTGGGGCGCGCGCGGATGTGGGGGCCCGCGCTGC 21
168 rGlnArgArgValArgPro 174
20 GCCAGCGCGCGCGCTGGCGCG 1

```

seq_name: gb_est36:AI873269

seq_documentation_block:

LOCUS AI873269 464 bp MRNA EST 01-SEP-1999

DEFINITION w41c08.x1 Soares.NFL_T_GBC.S1 Homo sapiens cDNA clone

IMAGE:2358158 3' similar to TR:015097 O15097 JAB, PARTIAL CDS ;

ACCESSION AI873269

VERSION AI873269.1 GI:5547318

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homidae; Homo.

alignment_scores:

Quality: 722.00 Length: 141
Ratio: 5.194 Gaps: 0
Percent Similarity: 98.582 Percent Identity: 97.163

alignment_block:
US-08-962-560A-4 x AA212316 ..

Align seg 1/1 to: AA212316 from: 1 to: 555

```

1 MetValAlaArgAsnGlnValAlaAlaAspAsnAlaIleSerProAlaAl 17
  |||||
133 ATGGAGAGCAGCAACAGAGTGGAGCCGACATCGATCTCCCGGAGCAGC 182
  |||||
17 AGLPProArgArgArgSerGluProSerSerSerSerSerSerSerp 34
  |||||
183 AGAGCCCGGAGCGGCGTCAGAGCCCTCCTCCTCCTCCTCCTCCTCCTC 232
  |||||
34 roAlaAlaProValArgProArgProArgProAlaValProAlaAla 50
  |||||
233 CAGGGGCCCCGCTGCTCCCGGCTGCTCCGCGGCTCCAGCCCGCAGCC 282
  |||||
51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArgAr 67
  |||||
283 CCTGGCGAGCTCACTTCCGACCTTCCGCTCCGCTCCGCTCCGCTCCGCT 332
  |||||
67 gIleThrArgThrSerAlaLeuLeuAspAlaCysGlyPheTyrTrpGly 84
  |||||
333 CATACGCGGAGCCAGCGCGCTCCTGAGCGCTGCGGCTTCTATTGGGGAG 382
  |||||
84 roLeuSerValHisGlyAlaHisGlyAlaArgLeuArgAlaGluProValGly 100
  |||||
383 CCCGAGAGCTGACAGGGGCGGACAGCGGCTGCTGCCGAGCCCGTGGC 432
  |||||
101 ThrPheLeuValAlaArgAspSerArgGlnArgAsnGlySphPheAlaLeu 117
  |||||
433 ACCTTCTTGGTGGCGGACAGTCCGACAGGAACTGCTTCCGCGCTCAG 482
  |||||
117 rValGlyMetAlaSerGlyProThrSerTleArgValHisPheGlnAla 134
  |||||
483 CCTGAAGATGGCTTGGGGCCAGAGACATCCGCTGCTCATTATGCCG 532
  |||||
134 lyArgPheHisLeuAspGlySer 141
  |||||
533 GGGCCTTCACTTGAGCGGACG 555
  |||||

```

seq_name: gb_est28:AI505924

seq_documentation_block:

LOCUS AI505924 417 bp mRNA EST 11-MAR-1999
DEFINITION vk69g08.x1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
IMAGE:559966 3' similar to IR:035716 035716 SUPPRESSOR OF CYTOKINE
SIGNALING-1. [1] ; mRNA sequence.

ACCESSION AI505924

VERSION AI505924.1 GI:4403775

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
1 (bases 1 to 417)
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

TITLE Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.

JOURNAL The WashU-NCI Mouse EST Project 1999
COMMENT On May 18, 1998 this sequence version replaced gi:3136451.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:548758
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Possible reversed clone: similarity on wrong strand
Seq primer: Primer name ambiguous
High quality sequence stop: 347.
Location/Qualifiers
1. 417
/organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:959966"
/clone_1lb="Knowles Solter mouse 2 cell"
/tissue="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pBluescribe (modified);
Site 1: Mui; Site 2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(drf): 5'-GGTGCAGCCGCGACCCCTTTTCTTTTCTTTT-3'.
were cloned into the Mui/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
BASE COUNT 51 a 162 c 135 g 69 t
ORIGIN

alignment_scores:
Quality: 718.00 Length: 139
Ratio: 5.319 Gaps: 0
Percent Similarity: 97.122 Percent Identity: 96.403

alignment_block:
US-08-962-560A-4 x AI505924 ..

Align seg 1/1 to: AI505924 from: 1 to: 417

```

42 ProCysProAlaValProAlaProAlaProGlyAspThrHisPheArgTh 58
  |||||
1 CCTGCGCGGCGGCTCCAGCCAGCCCTGCGGACACTTCCGCGAC 50
  |||||
58 rPheArgSerHisSerAspTyrArgArgGlyIleThrArgThrSerAlaLeu 75
  |||||
51 CTTCGCTCCCACTCCGATTACGGGGCATCACGGGAGACACGGGCTCC 100
  |||||
75 euAspAlaCysGlyPheTyrTrpGlyProLeuSerValHisGlyAlaHis 91
  |||||
101 TGGACCGCTGCGGCTTCTATTGGGAGCCCTCAGAGGTGACGCGGCGCAC 150
  |||||
92 GluArgLeuArgAlaGluProValGlyThrPheLeuValArgAspSerAr 108
  |||||
151 GAGCGGCTGCTGCGGAGCCGCTGGGACACTTCTTGGTGGCGGACAGTCG 200
  |||||
108 gGlnArgAsnCysPhePheAlaLeuSerValHisMetAlaSerGlyProT 125
  |||||
201 CCAAGGAACTGCTCTTCCGCTCAGCGTGAAGATGGCTTGGGCCCA 250
  |||||
125 hSerTleArgValHisPheGlnAlaGlyArgPheHisLeuAspGlySer 141
  |||||
251 CGAGCATCCGCGCTGCACTTCCAGCGGCGGCGCTTCCACTTGGACGCGCAGC 300
  |||||
142 ArgGluThrPheAspCysLeuPheGluLeuLeuGlnHisTyrValAlaAl 158
  |||||
301 CCGGAGACTTGTGACTGCTTTCAGCTGTGAGCACTACGTTGGCGGC 350
  |||||
158 aProArgArgMetLeuGlyAlaProLeuArgGlnArgArgValArgProL 175
  |||||
351 GCGCGCCGATGGGGGGGCGCGCTGCGGACGCGCGCGGCGCGC 400
  |||||

```

175 euglinc1eucysarg 180
|||||:|||||
401 TCGAGAGCTGTGTGCG 417

seq_name: gb_est38:AM048541

seq_documentation_block:

LOCUS AM048541 389 bp mRNA EST 18-SEP-1999
DEFINITION UI-M-BH1-alc-c-08-0-UI-s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
UI-M-BH1-alc-c-08-0-UI 3', mRNA sequence.

ACCESSION AM048541
VERSION AM048541.1 GI:5909070

KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
1 (bases 1 to 389) Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Bonaldo,M.F., Lennon,G. and Soares,M.B.

AUTHORS Normalization and subtraction: two approaches to facilitate gene
discovery

TITLE Genome Res. 6 (9), 791-806 (1996)

JOURNAL 97044477
COMMENT On Mar 9, 1998 this sequence version replaced g1:2946940.

CONTACT: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov

Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seq primer: M13 Forward

POLYA-NO.

FEATURES Location/Qualifiers

SOURCE

1..389 /organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-BH1-alc-c-08-0-UI"

/clone_lib="NIH_BMAP_M_S2"

/dev_stage="27-32 days"

/note="Vector: pRT3D-Pac (Pharmacia)"

/lab_host="DH10B (Life Technologies)"

/polylinker="Site_1: Not I; Site_2: Eco RI; The

NIH_BMAP_M_S2 library is a subtracted library derived from

NIH_BMAP_M_S1, which in turn is a subtracted library

derived from a mixture of normalized libraries from ten

regions of the mouse brain (cerebellum, brain stems,

olfactory bulbs, hypothalamus, cortex, amygdala, basal

ganglia, pineal gland, striatum, hippocampus). The driver

used for subtraction consisted of a pool of 5,000 clones

from the NIH_BMAP_M_S1 library and a pool of 2,000 clones

obtained from non-normalized and normalized mouse brain

spinal cord libraries.

TAG_LIB=NIH_BMAP_M_S2

TAG_TISSUE=corpus striatum

TAG_SEQ=ACGCGC

BASE COUNT 65 a 123 c 151 g 50 t
ORIGIN

alignment_scores: Quality: 687.00 Length: 129
Ratio: 5.326 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.225

alignment_block:

US-08-962-560A-4 x AM048541/rev ..

Align seg 1/1 to reverse of: AM048541 from: 1 to: 389

46 ValProAlaProAlaProGlyAspThrHisPheArgThrPheArgSerHis 62
|||||:|||||
387 GTCCCAACCCCGCCGCTGGCGACACTCCTCCGACCTCCGCTCCCA 338
62 sSerAspTyrArgArgGlierArgThrSerAlaLeuAlaPalacyg 79
|||||:|||||
337 CTCGATTACCGCGCATCAGCGGACGCGCTCTGAGCGCTCGC 288
79 LpPheTyrTrpGlyProLeuSerValHisGlyAlaHisGluArgLeuArg 95
|||||:|||||
287 GCTTCTATTGGGGACCCCTGACGCTGCACGGGGCCGACGAGCGCTGCT 238
96 AlaGluProValGlyThrPheLeuValArgAspSerArgGlnArgAsnCy 112
|||||:|||||
237 GCCGAGCCCGCTGGCACCCTTCTGTGGCGGACAGTCCCAAGCACTG 188
112 sPhePheAlaLeuSerValLysMetAlaSerGlyProThrSerIleArgV 129
|||||:|||||
187 CTTCTTCGGCGCTCAGCGTGAAGATGCTTCGGGCCCCAGACATCCCG 138
129 aHisPheGlnAlaGlyArgPheHisLeuAspGlySerArgGluThrPhe 145
|||||:|||||
137 TCCACTTCCAGCGCGCGCTTCCACTTGGAGCGGACCGCGAGACTTC 88
146 AspCysLeuPheGluLeuLeuGluHisTyrValAlaAlaProArgArgme 162
|||||:|||||
87 GACTGCTTTCGAGCTGCTGTGAGCAGTACGAGCGGCGCGCGCAT 38
162 tLeuGlyAlaProLeuArgGlnArgArgValArgpro 174
|||||:|||||
37 GTTGGGGGCGCGCGTCCGACGCGCGCGCTGGCGCGC 1

seq_name: gb_est28:A1502911

seq_documentation_block:

LOCUS A1502911 393 bp mRNA EST 11-MAR-1999
DEFINITION UI-R-C1-Kn-f-07-0-01-s1 UI-R-C1 Rattus norvegicus cDNA clone
UI-R-C1-Kn-f-07-0-01 3', mRNA sequence.

ACCESSION A1502911

VERSION A1502911.1 GI:4400762

KEYWORDS EST.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 393) Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
discovery

TITLE Genome Res. 6 (9), 791-806 (1996)

JOURNAL 97044477

COMMENT On Mar 10, 1998 this sequence version replaced g1:2948661.

CONTACT: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through
Research Genetics (www.reagen.com)

Seq primer: M13 Forward.

FEATURES Location/Qualifiers

SOURCE

1..393 /organism="Rattus norvegicus"

/strain="Sprague-Dawley"

```

/bb_xref="taxon:10116"
/clone="UI-R-C1-ka-f-07-0-UI"
/clone.lib="UI-R-C1"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI. The UI-R-C1
library is a subtracted library derived from the UI-R-C0
library, which is a subtracted library derived from the
UI-R-A1 and UI-R-R1 libraries. The UI-R-A1 library
consisted of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The UI-R-E1 library consisted of a mixture of
individually tagged normalized libraries constructed from
8, 12 and 18-day embryo. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dr track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-C1) was constructed as follows: PCR
amplified cDNA inserts from UI-R-C0 clones from which 3'
ESTs had been derived was used as a driver in a
hybridization with the UI-R-C0 library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-C1
library. This procedure has been previously described
(Bonaldi, Lennon and Soares, Genome Research 6: 791-806,
1996)."

```

BASE COUNT 66 a 128 c 149 g 50 t
ORIGIN

alignment_scores:
Quality: 680.00 Length: 127
Ratio: 5.354 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-962-560A-4 x A1502911/rev ..

Align seg 1/1 to reverse of: A1502911 from: 1 to: 393

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48 AAlaProAlaProGlyAspThrHisPheArgThrPheArgSerHisSerAs 64
|||||
381 GCCCGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 332
64 PTYRARGTGLIETHRARGTHRSERALALEULAUASPALACYSGLYPHET 81
|||||
331 TTACCGGCGCATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCT 282
81 YTRPGIYPRoleuservAlHisGlyAlaHisGlyAlaGlyLeuArgAlaGlu 97
281 ACTGGGACCCCTGAGCGTGCATGGGCGGCGGCGGCGGCGGCGGCGGAG 232
98 ProValGlyThrPheLeuValArgAspSerArgGlnArgAspCysPheph 114
231 CCCGTGGGCGACTTCTTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 182
114 GAlaLeuSerValLysMetAlaSerGlyProThrSerIleArgValHisP 131
181 CGCGCTACGCGTGAAGATGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGG 132
131 heGlnAlaGlyArgPheHisLeuAspGlySerArgGluThrPheAspys 147
131 TCCAGGCGCGCGCTTCCACCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 82
148 LeuPheGluLeuLeuGluHisTyrValAlaAlaProArgArgMetLeuG1 164
81 CTCTTGAGACTGCTGAGACACTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 32

```

164 YAlaProLeuArgGlnArgValArgPro 174
|||||
31 GCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1

seq_name: gb_est16:AA547459

seq_documentation_block:
LOCUS AA547459 475 bp mRNA
DEFINITION VK69G08.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
IMAGE:59966 5', mRNA sequence.
ACCESSION AA547459
VERSION AA547459.1 GI:2308750
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 475)
Matra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucada, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
JOURNAL
COMMENT
The WashU-HMNI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gl:692678.
Contact: Matra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
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Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.lml.gov) for further information.
MGI:548758
High quality sequence stop: 289.

FEATURES
SOURCE
Location/Qualifiers

1..475
/organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:959966"
/clone.lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pBluescribe (modified);
site_1: MluI; site_2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(dT): 5'-CGGTGACCGTCGACCGCTTTTCTTTTCTTT-3'.
were cloned into the MluI/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
BASE COUNT 64 a 171 c 148 g 92 t
ORIGIN

alignment_scores:
Quality: 607.00 Length: 159
Ratio: 4.245 Gaps: 3
Percent Similarity: 89.937 Percent Identity: 88.050

alignment_block:

US-08-962-560A-4 x AA547459 ..

Align seg 1/1 to: AA547459 from: 1 to: 475

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54 ThrHisPheArgThrPheArgSerHisSerAspTyrArgArgIleThrArg 70
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2 ACTCACTTCCGACACTTCCGCTCCGATTCGATACCGGCGGCGGCGGCGGCGG 51
70 gThrsAlaLeuLeuAspAlaCysGlyPheTyrTrrPglyProLeuServ 87

```

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52 GACCGCCGCTCTCGAGCGCTGCGG..TTCTATTGGGAGACCTTG..AGCG 99
87 aLHISGLVAlaHISGLuArgLeuArgAlaGluProValGlyThrPheLeu 103
100 TGCAGGGGGCGCAGAGCGGCTGCTGCCGAGCCCGTGGACCTTCTTG 149
104 ValArgAspSerArgGlnArgAsnGlyPheAlaLeuSerValLysMe 120
150 TCGCGACAGCTCG...CAACGGAAGTCTCTTCTCGCGCTCAC..GTGAAGAT 195
120 tAlaSerGlyProThrSerIleArgValHisPheGlnAlaGlyArgPhe 137
196 GGCCTTGGGGCCCGACAGCATCCGGCTGCACCTCCAGGCGCGCGCTTCC 245
137 IsLeuAspGlySerArgGluThrPheAspCysLeuPheGluLeuGlu 153
246 ACTTGGACGCGCAGCCGCGAGACCTTGCAGCTGCTTTCGAGCTGCTGAG 295
154 HistyrValAlaAlaProArgArgMetLeuGlyAlaProLeuArgGlnAr 170
296 CACTACGTGGCGCG...CGCGGATGTGGGGCGCGCTGCGCAGCGCGCG 342
170 gArgValArgProLeuGlnGluLeuGlyArgGlnArgIleValAlaAlaY 187
343 TGC.....GCGCTGCAGAGAGCTGTGTGCCAGCGCATGTGGCGCGCG 385
187 aLIGYArgGluAsnLeuAlaArgIleProLeuAsnProValLeuArgAsp 203
386 TGGGTTCGGAGAACCTTGGCGCGCATCCCTCTTAACCGGTACTCGTGAC 435
204 TyrLeuSerSerPheProPheGlnIle 212
436 TACCTGAGTTCTTCCCTTCCAGATC 462
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